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Fax Cover Sheet

Date: 28 Sep 2004

5 Pgs

| | |
|--|--------------------------------|
| To: Dr. Stuart Macphail | From: Maher M. Haddad |
| Application/Control Number: 09/787,097 | Art Unit: 1644 |
| Fax No.: (617) 542-8906 212-258-2291 | Phone No.: (571) 272-0845 |
| Voice No.: 212-641-2215 | Return Fax No.: (703) 273-0845 |
| Re: | CC: |
| <input type="checkbox"/> Urgent <input type="checkbox"/> For Review <input type="checkbox"/> For Comment <input type="checkbox"/> For Reply <input checked="" type="checkbox"/> Per Your Request | |

Comments:

Stuart,

Enclosed please find a couple of references that would read on the nucleic acid comprising a sequence encoding a fusion protein comprising the antigenic fragment and a heterologous sequence. Adams et al teaches a 396 nucleic acid sequence that encodes 86 amino acid seq of SEQ ID NO: 12 and a heterologous sequence. Also, Bonaldo et al teaches a 435 nucleic acid sequence comprising a sequence encoding a fusion protein comprising a fragment of a 76 amino acid in length and a heterologous sequence. The prior art reads on claims 6, 47, 48 and 60-65.

Maher Haddad

Maher Haddad

Number of pages __ including this page

STATEMENT OF CONFIDENTIALITY

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Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

163 GlucyGlnProAsnArgIleMetArgLeuArgPheAsnHisPheAlaThrGluCysSer 182
165 GAAGGACGAGCAATGAAATGAGACTTCGCTTCAACATTTTCTACAGATGATGAC 224
183 TtpAspHisLeuTyValTyAspGlyAspSerIleTyAlaProLeu 198
225 TGGGACCATTTATATGTTTATGATGGGACTCAATCTAGCACCTCTG 272

SULT 61
120845
CUS
FINITION
UI-M-BH2.3-aca-e-06-0-UI.s1 NIH BMAP M.S3.3 Mus musculus cDNA clone
UI-M-BH2.3-aca-e-06-0-UI 3', mRNA sequence.
AW120845
RSION
YWORDS
URCE
ORGANISM
Mus musculus (house mouse)
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 435)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
8889548
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: NIH BMAP cDNA clones will be made
available by the means that is soon to be determined. When NIH
determines the means for distribution of the BMAP cDNA clones, this
record will be updated accordingly when that means is determined.
Seq primer: M13 Forward
POLYA=No.

Location/Qualifiers
1. 435
/organism="Mus musculus"
/mol type="mRNA"
/strain="C57BL/6J"
/db xref="taxon:10090"
/clone="UI-M-BH2.3-aca-e-06-0-UI"
/dev stage="27-32 days"
/lab host="DH10B (Life Technologies)"
/clone lib="NIH BMAP M.S3.3"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The
NIH BMAP M.S3.3 library is a subtracted library of a
series, ultimately derived from a mixture of individually
tagged normalized libraries from ten regions of the mouse
brain (cerebellum, brain stems, olfactory bulbs,
hypothalamus, cortex, amygdala, basal ganglia, pineal
gland, striatum, hippocampus) after a series of
subtractions to reduce the representation of cDNAs from
which ESTs had already been generated. The following
serially subtracted libraries were generated in this
process: NIH BMAP M.S3.3, NIH BMAP M.S2, NIH BMAP M.S1.
The subtracted library (NIH BMAP M.S3.3) was constructed
as follows: PCR amplified cDNA inserts from NIH BMAP M.S2
clones from which 3' ESTs had been derived was used as a
driver in a hybridization with the NIH BMAP M.S2 library
in the form of single-stranded circles. The remaining
single-stranded circles (subtracted library) was purified
by hydroxyapatite column chromatography, converted to
double-stranded circles and electroporated into DH10B
bacteria (Life Technologies) to generate the

FEATURES
source

ORIGIN

Alignment Scores:
Pred. No.: 3,176-51 Length: 435
Score: 76.00 Matches: 76
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.32% Indels: 0
DB: 10 Gaps: 0

US-09-787-097-12 (1-1429) x AW120845 (1-435)

QY 123 GlyTyrValGluGlnCysGlnHisCysGlyArgPheArgLeuThrGlySerSer 142
Db 44 GGTGGTGGGCGAGCAATGCGACCTCGCGGGCGGCTTCAGACTAACTGGCTCTCT 103
QY 143 GlyPheValThrAspGlyProGlyAsnTyIlystTyIlystCysThrTyrLeuile 162
Db 104 GGATTTGTAACAGATGGACCTGGGAAATTATAATATAAGACGAGTGCATGGCTCAT 163
QY 163 GluGlyGlnProAsnArgIleMetArgLeuArgPheAsnHisPheAlaThrGluCysSer 182
Db 164 GAAGGACGAGCAATGAAATGAGACTTCGCTTCAACATTTTCTACAGATGATGAC 223
QY 183 TtpAspHisLeuTyValTyAspGlyAspSerIleTyAlaProLeu 198
Db 224 TGGGACCATTTATATGTTTATGATGGGACTCAATCTAGCACCTCTG 271

RESULT 62

BI202684

LOCUS

DEFINITION

UI-M-CG0p-brk-h-05-0-UI.s1 NIH BMAP Ret4 S2 Mus musculus cDNA clone

UI-M-CG0p-brk-h-05-0-UI 3', mRNA sequence.

ACCESSION

BI202684

VERSION

EST

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 435)

Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

97044477

8889548

Contact: Chin, H

National Institute of Mental Health

6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD

20892-9643, USA

Tel: 301 443 1706

Fax: 301 443 9890

Email: mEST@mail.nih.gov

Oligo-dT track not found, Not I site shown in beginning of sequence

is likely internal to the message. cDNA Library Preparation: M.B.

Soares Lab Clone distribution: Researchers may obtain BMAP cDNA

clones from RESEARCH GENETICS. It should be noted that Bento Soares

is generating a small number of additional specialized

non-redundant arrays of BMAP cDNAs whose availability will be

considered under appropriate and limited collaborative arrangements

The tissue for this library was contributed by Dr. Xin-Yuan Fu,

Yale University School of Medicine

Seq primer: M13 Forward

POLYA=No.

Location/Qualifiers

1. 435

source

NIH BMAP M.S3.3 library. This procedure has been
previously described (Bonaldo, Lennon and Soares, Genome
Research 6:791-806, 1996)
TAG_TISSUE=hypothalamus
TAG_LIB=NIH BMAP M.S3.3
TAG_SEQ=CGGTA

Alignment Scores:
Pred. No.: 3,176-51 Length: 435
Score: 76.00 Matches: 76
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.32% Indels: 0
DB: 10 Gaps: 0

US-09-787-097-12 (1-1429) x AW120845 (1-435)

QY 123 GlyTyrValGluGlnCysGlnHisCysGlyArgPheArgLeuThrGlySerSer 142
Db 44 GGTGGTGGGCGAGCAATGCGACCTCGCGGGCGGCTTCAGACTAACTGGCTCTCT 103
QY 143 GlyPheValThrAspGlyProGlyAsnTyIlystTyIlystCysThrTyrLeuile 162
Db 104 GGATTTGTAACAGATGGACCTGGGAAATTATAATATAAGACGAGTGCATGGCTCAT 163
QY 163 GluGlyGlnProAsnArgIleMetArgLeuArgPheAsnHisPheAlaThrGluCysSer 182
Db 164 GAAGGACGAGCAATGAAATGAGACTTCGCTTCAACATTTTCTACAGATGATGAC 223
QY 183 TtpAspHisLeuTyValTyAspGlyAspSerIleTyAlaProLeu 198
Db 224 TGGGACCATTTATATGTTTATGATGGGACTCAATCTAGCACCTCTG 271

RESULT 62
BI202684
LOCUS
DEFINITION
UI-M-CG0p-brk-h-05-0-UI.s1 NIH BMAP Ret4 S2 Mus musculus cDNA clone
UI-M-CG0p-brk-h-05-0-UI 3', mRNA sequence.
ACCESSION
BI202684
VERSION
EST
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 435)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
8889548
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
clones from RESEARCH GENETICS. It should be noted that Bento Soares
is generating a small number of additional specialized
non-redundant arrays of BMAP cDNAs whose availability will be
considered under appropriate and limited collaborative arrangements
The tissue for this library was contributed by Dr. Xin-Yuan Fu,
Yale University School of Medicine
Seq primer: M13 Forward
POLYA=No.
Location/Qualifiers
1. 435
source

Pred. No.: 5,98e-62 Length: 281
 Score: 89.00 Matches: 89
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 6.23% Indels: 0
 DB: 10 Gaps: 0

US-09-787-097-12 (1-1429) x BG015062 (1-281)

QY 588 SerAspPheMetAlaTyrAspIleAlaCysAspArgTyrSerValLeuProArgProAsp 607
 Db 279 TCAGATTTCATGGCTATGACATTCCTGTCGACCGTGGTCAGTCTCCACAGCTGAT 220
 QY 608 LeuHisHisAspValAsnArgPheGlyHisSerIleValLeuHisAsnSerThrMetTyr 627
 Db 219 CTCACCATGATGTCACAGATTTGGCATTTCACAGCATCTTCACACAGCACCATGAT 160
 QY 628 ValPheGlyGlyPheAsnSerLeuLeuSerAspIleLeuValPheThrSerGluGln 647
 Db 159 GGTTCGGTGGTTCATAGTCTCTCTCAGCGACATCTGGTATTCACCTCGGAACAG 100
 QY 648 CysAspAlaHisArgSerGluAlaAlaCysLeuAlaIleGlyProGlyIleArgCysVal 567
 Db 99 TGTGATGGCATCGAGGAGGCGCTGTATTAGCAGCAGGACCTGTTATCGGTGTG 40
 QY 668 TrpAsnThrGlySerSerGlnCysIle 676
 Db 39 TGGAACACAGCGTCTCTCACTGTATC 13

RESULT 51

BF853021/c 483 bp mRNA linear EST 16-JAN-2001
 LOCUS BF853021-191200-001-g05 EN0093 Homo sapiens cDNA, mRNA sequence.

DEFINITION

MR2-EN0093

ACCESSION

BF853021

VERSION

BF853021.1 GI:12240869

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., de Oliveira, F.S., Bucher, P., Jongeneel, C.V.,

O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE

20202653

PUBMED

10737800

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the PAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR2&t2=MR2-EN0093-

191200-001-g05&t3=2000-12-19&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 483.

FEATURES

Location/Qualifiers

1..483

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="EN0093"

/notes="Organ: lung normal; Vector: puc18; Site: 1: SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.: 1,02e-61 Length: 483
 Score: 89.00 Matches: 89
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 6.23% Indels: 0
 DB: 10 Gaps: 0

US-09-787-097-12 (1-1429) x BF853021 (1-483)

QY 1141 GluValGluAsnArgTyrGlnGlyAsnProLeuArgGlyThrCysTyrTyrThrLeuLeu 1160
 Db 446 GAGTAGAATCGATACCAAGGAACCTCTCAGAGGAACATGTTATTATATCTCTT 387
 QY 1161 IleAspTyrGlnPheThrPheSerLeuSerGlnGluAspArgTyrTyrThrAlaIle 1180
 Db 386 ATTGACTATCAGTTCACCTTACTCTATCCAGGAAGATGATCGCTATTACACAGCTATC 327
 QY 1181 AsnPheValAlaThrProAspGlnGlnAsnArgAspLeuAspMetPheIleAsnAlaSer 1200
 Db 326 AATTGTGCTACTCTCTGACGAACAAACAGGATTTGCAATGTCATCAATGCTCC 267
 QY 1201 LysAsnPheAsnLeuAsnIleThrTyrAlaAlaSerPheSerAlaGlyThrGlnAlaGly 1220
 Db 266 AAGAATTCAACCTCAACATCAGCTGGGTGCGAGTTTCTCAGCTGGAACCCAGGCTGGA 207
 QY 1221 GluGluMetProValValSerLysThr 1229
 Db 206 GAAGAGATGCTGTGTTCATAAACC 180

RESULT 52

AA350292

LOCUS

AA350292 396 bp mRNA linear EST 21-APR-1997

DEFINITION

EST57511 Infant brain Homo sapiens cDNA 3' end, mRNA sequence.

ACCESSION

AA350292

VERSION

AA350292.1 GI:2002619

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 396)

Adams, M.D., Kerlavage, A.R., Fields, C. and Venter, J.C.

3,400 expressed sequence tags identify diversity of transcripts

from human brain

Nat. Genet. 4, 256-267 (1993)

93364420

JOURNAL

Pubmed

MEDLINE

8358434

COMMENT

Other ESTs: EST57512, THCI68885

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlav@tigr.org

For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene

Index (http://www.tigr.org/cdb/hgi/hgi.html)

Seq primer: M13-21.

Location/Qualifiers

1..396

/organism="Homo sapiens"

/mol_type="mRNA"

FEATURES

source

/db_xref="ATCC (inhost):151062"
 /db_xref="taxon:9606"
 /sex="female"
 /dev_stage="infant"
 /clone_lib="infant brain"
 /note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
 Site_2: NotI"

ORIGIN

Alignment Scores:
 Pred. No.: 2,26e-59 Length: 396
 Score: 86.00 Matches: 123
 Percent Similarity: 98.40% Conservatives: 0
 Best Local Similarity: 98.40% Mismatches: 1
 Query Match: 6.02% Indels: 2
 DB: 9 Gaps: 0

US-09-787-097-12 (1-1429) x AA350292 (1-396)

QY 480 TyrAspLeuAspLysAsnThrTrpSerIleLeuHisThrGlnGlyAlaLeuValGlnGly 499
 Db 1 TATGATTGGTATAGAACACATCGAGTATATTACACCCAGGGTCCCTTGTGCAAGG 60
 QY 500 GlyTrpGlyHisSerValTyAspHisArgThrArgAlaLeuTyValHis-GlyCl 519
 Db 61 GGTACGGCCCATACGACGTGTTCAGCACCATAGGACGAGGCGCCCTATACGTTNA-TGGTGG 119
 QY 519 YTyLysAlaPheSerAlaAsnLysTyArgLeuAlaAspAspLeuTyArgTyAspVa 539
 Db 120 CTACAGGCTTTCAGTCCCAATAGTACCGGCTTCGAGATGATCTCTACCGATATAGT 179
 QY 539 LaspThrClnMetTrpThrIleLeuLysAspSerArgPheArgTyLeuHisThrAl 559
 Db 180 GATACCCAGATGGACCATCTTAAGGACACCCGATTTTCGGTACTTCACACAGC 239
 QY 559 aValIleValSerGlyThrMetLeuValPheGlyGlyAsnThrHisAspAspThrSerWe 579
 Db 240 TGTGATAGTGGTGGACCATGCTGGTGTGTTGGAGGAACACACACATGACATCAT 299
 QY 579 tSerHisGlyValLysCysPheSerAspPheMetAlaTyAspIleAlaCysAspAr 599
 Db 300 GAGCGATGGCGCCAAATGCTCTTCAGATTTTCATGGGCTATGACATGGCTGTGACCG 359
 QY 599 gTtpSerValLeu 603
 Db 360 CTGGTCAGTGCTT 372

RESULT 53
 CE522182
 LOCUS
 DEFINITION UI-M-GH0-cep-c-09-0-UI.r1 NIH_BMAP_GH0 Mus musculus cDNA clone
 IMAGE:6842530 5', mRNA sequence.
 CE522182
 CE522182.1 GI:29355537
 EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
 http://genome.uiowa.edu/distribution/mousefl.html
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)

FEATURES

Location/Qualifiers
 1..758
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CS7BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:6842530"
 /tissue_type="Whole brain"
 /dev_stage="1, 5, and 15 days newborn"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH BMAP_GH0"
 /note="Organ: Brain; Vector: pYX-Asc; Site_1: EcoR I;
 Site_2: Not I; The library was constructed according
 Bonaldi, Lennon and Soares, Genome Research, 5:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with EcoR I adaptor, digested with NotI and then cloned
 directionally into pYX-Asc vector. The library tag
 sequence located between the Not I site and the PolyA tail
 is CCACTGAAAT. This library was created for the University
 Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
 program coordinator."

ORIGIN

Alignment Scores:
 Pred. No.: 1,78e-57 Length: 758
 Score: 84.00 Matches: 84
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.88% Indels: 0
 DB: 14 Gaps: 0

US-09-787-097-12 (1-1429) x CB522182 (1-758)

QY 1346 GlyGlySerIleLysThrValProLysProIleAlaLeuLysProCysPheGlyAsnLys 1365
 Db 15 GGGGGAAGTATAAGACCGTTCCTAAGCCCATTCCTCGAGCCCTGCTTTGTACAA 74
 QY 1366 AlaAlaValLeuSerValPheValArgLeuProArgGlyLeuGlyGlyLeuProPro 1385
 Db 75 GCGGAGTCTCTCTCTGTTATTCGTGAGGCTCTCTGAGAGGATCCCTCTCTCT 134
 QY 1386 GlyGlnSerGlyLeuAlaValAlaSerAlaLeuValAspIleSerGlnMetProIle 1405
 Db 135 GGTCACTAGGCTCGCTGTGCGCAGTCCCTGCTGACATTTCTCAGCAGATGCCAATA 194
 QY 1406 ValTYLysGlyLysSerGlyValAlaValArgAsnArgLysGlnGlnProAlaGlnPro 1425
 Db 195 GTGTACAGGAGAGTCTAGGAGCTGTAAAGAACCGGAGGACGAGCGGCTGTGACAGCT 254
 QY 1426 GlyThrCysIle 1429
 Db 255 GGAACCTGCATT 266

RESULT 54
 CE531905
 LOCUS
 DEFINITION AGENCOURT 10205588 NIH_MGC_126 Homo sapiens cDNA clone
 IMAGE:655819 5', mRNA sequence.
 CE531905
 CE531905.1 GI:22842346
 ACCESSION
 VERSION
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 778)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/

```

/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-BH2.1-apk-d-10-0-UI"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NIH_BMAP_Ret4_S2"
/notes="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The
NIH_BMAP_Ret4_S2 library is a subtracted library,
ultimately derived from mouse retina tissue libraries at
various stages of development. For a detailed description
of the library from which this clone was derived, please
visit our web site at brainet.english.yale.edu. The tissue
for this library was contributed by Dr. Xin-Yuan Fu, Yale
University School of Medicine
TAG_SEQ=None found"

```

ORIGIN

```

Alignment Scores:
Pred. No.: 3,17e-51 Length: 488
Score: 76.00 Matches: 76
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.32% Indels: 0
DB: 12 Gaps: 0

US-09-787-097-12 (1-1429) x B1202684 (1-435)

QY 123 GlyTyrValGlyGluGlnCysGlnHisCysGlyGlyArgPheArgLeuThrGlySerSer 142
Db 45 GCGTGGGTGGCGAGCAATGCCAGCACTCGGGGGCGGCTTCAGACTTACGCTCTCT 104
QY 143 GlyPheValThrAspGlyProGlyAsnTyrLysTyrLysThrLysCysThrTrpLeuLeu 162
Db 105 GGAATTGTACAGATGCGCTGGGAATTATATATAGAGAGAGTGCATGGCTCAT 164
QY 163 GluGlyGlnProAsnArgIleMetArgLeuArgPheAsnHisPheAlaThrGluCysSer 182
Db 165 GAAGGACAGCAATAGATAATAGAGACTTCGCTTCAACCATTTTCTACAGATGAGC 224
QY 183 TrpAspHisLeuTyrValTyrAspGlyAspSerIleTyrAlaProLeu 198
Db 225 TGGGACCATTTATATGTTTATGATGGGAGTCAATCTACGACCTCTG 272

```

RESULT 63

```

AW124828
LOCUS
DEFINITION
UI-M-BH2.1-apk-d-10-0-UI-s1 NIH_BMAP_M_S3.1 Mus musculus cDNA clone
UI-M-BH2.1-apk-d-10-0-UI 3', mRNA sequence.
ACCESSION
AW124828
VERSION
AW124828.1 GI:6100358
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 488)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalisation and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL
97044477
MEDLINE
PUBMED
8889548
COMMENT
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: nst@mail.nih.gov
Oligo-dt track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.

```

Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined. Seq primer: M13 Forward POLYA-No.

FEATURES

source

Location/Qualifiers

1..488

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clones="UI-M-BH2.1-apk-d-10-0-UI"

/dev stage="27-32 days"

/lab_host="DH10B (Life Technologies)"

/clone_lib="NIH_BMAP_M_S3.1"

/notes="Vector: p773D-Pac (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; The

NIH_BMAP_M_S3.1 library is a subtracted library of a

series, ultimately derived from a mixture of individually

tagged normalized libraries from ten regions of the mouse

brain (cerebellum, brain stems, olfactory bulbs,

hypothalamus, cortex, amygdala, basal ganglia, pineal

gland, striatum, hippocampus) after a series of

subtractions to reduce the representation of cDNAs from

which ESTs had already been generated. The following

serially subtracted libraries were generated in this

process: NIH_BMAP_M_S3.1, NIH_BMAP_M_S2, NIH_BMAP_M_S1.

The subtracted library (NIH_BMAP_M_S3.1) was constructed

as follows: PCR amplified cDNA inserts from NIH_BMAP_M_S2

clones from which 3' ESTs had been derived was used as a

driver in a hybridization with the NIH_BMAP_M_S2 library

in the form of single-stranded circles. The remaining

single-stranded circles (subtracted library) was purified

by hydroxyapatite column chromatography, converted to

double-stranded circles and electroporated into DH10B

bacteria (Life Technologies) to generate the

NIH_BMAP_M_S3.1 library. This procedure has been

previously described (Bonaldo, Lennon and Soares, Genome

Research 6:791-806, 1996)

TAG_TISSUE=amygdala

TAG_LIB=NIH_BMAP_M_S3.1

TAG_SEQ=GTGAG

ORIGIN

```

Alignment Scores:
Pred. No.: 3,55e-51 Length: 488
Score: 76.00 Matches: 76
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.32% Indels: 0
DB: 10 Gaps: 0

```

US-09-787-097-12 (1-1429) x AW124828 (1-488)

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QY 123 GlyTyrValGlyGluGlnCysGlnHisCysGlyGlyArgPheArgLeuThrGlySerSer 142
Db 44 GCGTGGGTGGCGAGCAATGCCAGCACTCGGGGGCGGCTTCAGACTTACGCTCTCT 103
QY 143 GlyPheValThrAspGlyProGlyAsnTyrLysTyrLysThrLysCysThrTrpLeuLeu 162
Db 104 GGATTGTGACAGATGACCTGGGAATTATAAATATAGAGAGTGCATGGCTCAT 163
QY 163 GluGlyGlnProAsnArgIleMetArgLeuArgPheAsnHisPheAlaThrGluCysSer 182
Db 164 GAAGGACAGCAATAGATAATAGAGACTTCGCTTCAACCATTTTCTACAGATGAGC 224
QY 183 TrpAspHisLeuTyrValTyrAspGlyAspSerIleTyrAlaProLeu 198
Db 224 TGGGACCATTTATATGTTTATGATGGGAGTCAATCTACGACCTCTG 271

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RESULT 64

BS952846